IN THE SPECIFICATION:

Please amend paragraph starting on page 41, line 36 as follows:

Ile 689 from the peptide interacts with three receptor residues (Asp 538, Glu 542 and Leu 539). The γ-carboxylate of Glu 542 forms hydrogen bonds to the amides of residues 689 and 690 of the peptide. A water-mediated hydrogen bond network is formed between the imidazole ring of His 377, the γ-carboxylate of Glu 380, and the amide of Tyr 537. Three residues (Glu 380, Leu 536 and Tyr 537) interact with each other through van der Waals contacts and/or hydrogen bonds. Intriguingly, mutations in each these three residues dramatically increase the transcription activity of unliganded ERα LBD (Eng, *et al.*, *Mol. Cell. Biol.* (1997) 17:4644-4653); Lazennec, et al., *Mol Endocrinol.* (1997) 11:1375-86; White, *et al.*, *EMBO J.* (1997) 16:1427-35). Atomic coordinates of DES-LBD-peptide complex are attached as Appendix 2. The structure in Appendix 2 comprises: a portion of human ERα, residues 305 – 549 of chain A (SEQ ID NO: 56), and residues 305 – 549 of chain B (SEQ ID NO: 57); two molecules of DES; and two molecules of GRIP-1 NR-box 2 peptide, chain C (SEQ ID NO: 58) and chain D (SEQ ID NO: 60). still new matter